

What is claimed is:

1. A process for determining whether or not a test sample originating from or containing human cells has a tumor progression potential, wherein a second sample originating from non-tumor cells from the same individual or a different individual of the same species is also used, which process comprises the following steps:
  - (a) incubating said samples under stringent hybridization conditions with a nucleic acid probe which is selected from the group consisting of:
    - (i) a nucleic acid with a sequence of SEQ ID NO:1 or a fragment thereof;
    - (ii) a nucleic acid with a sequence which is complementary to any nucleic acid of (i);
    - (iii) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and
    - (iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and
  - (b) determining the approximate amount of hybridization of each respective sample with said probe and
  - (c) comparing the approximate amount of hybridization of the test sample to an approximate amount of hybridization of said second sample to identify whether or not the test sample contains a lower amount of the nucleic acid than does said second sample.
2. A process for determining whether or not a test sample originating from or containing human cells has a tumor progression potential, which process comprises the following steps:
  - (a) incubating a first compartment of said sample under stringent hybridization conditions with a first nucleic acid probe which is selected from the group consisting of:
    - (i) a nucleic acid with a sequence of SEQ ID NO:1 or a fragment thereof;

- (ii) a nucleic acid with a sequence which is complementary to any nucleic acid of (i);
  - (iii) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (i); and
  - (iv) a nucleic acid with a sequence which hybridizes under stringent conditions with the nucleic acid of (ii); and
- (b) incubating a second compartment of said sample under stringent hybridization conditions with a second nucleic acid probe being a housekeeping gene or a fragment thereof;
  - (c) determining the approximate amount of hybridization of said sample with said first and second probe;
  - (d) identifying whether or not the test sample contains an at least 3-fold amount of nucleic acid hybridizing with the first probe in comparison to the amount of nucleic acid hybridizing with the second probe.